

STN Search Summary
09/963790

=> d his

FILE 'CAPLUS' ENTERED AT 16:25:47 ON 04 DEC 2003
L1 313 S DEAD (S) HELICASE
L2 2 S L1 AND (CORYNEFORM OR GLUTAMICUM)
L3 1035524 S 1-2

L2 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2003:376895 CAPLUS
DN 138:380486
TI Corynebacterium SES (genetic stability, gene expression and protein secretion) genes and their use for enhancing production of fine chemicals
IN Zelder, Oskar; Pompejus, Markus; Schroeder, Hartwig; Kroeger, Burkhard; Klopprogge, Corinna; Haberhauer, Gregor
PA BASF Aktiengesellschaft, Germany
SO PCT Int. Appl., 265 pp.
CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003040180	A2	20030515	WO 2002-EP12138	20021031
	DE 10154180	A1	20030515	DE 2001-10154180	20011105
PRAI	DE 2001-10154180	A	20011105		

L2 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2002:256307 CAPLUS
DN 136:293612
TI Sequence of dead gene from corynebacteria and use thereof in synthesis of L-lysine
IN Farwick, Mike; Huthmacher, Klaus; Brehme, Jennifer; Pfefferle, Walter
PA Degussa A.-G., Germany
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002026787	A1	20020404	WO 2001-EP10772	20010918
	DE 10047865	A1	20020418	DE 2000-10047865	20000927
	AU 2001093821	A5	20020408	AU 2001-93821	20010918
	EP 1320544	A1	20030625	EP 2001-974264	20010918
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	US 2002115161	A1	20020822	US 2001-963790	20010927
PRAI	DE 2000-10047865	A	20000927		
	WO 2001-EP10772	W	20010918		

SEQUENCE SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 17:12:34 ; Search time 8732 Seconds
(without alignments)
11155.041 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapext 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:

```

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				ID	Description
	No.	Score	Match	Length	DB	
1	2381	100.0	2381	6	AX404864	Appl. WO
2	2377.8	99.9	333150	1	AP005277	GenBank
3	2377.8	99.9	349980	6	AX127146	EPN 1108790
4	2377.8	99.9	349980	6	AX127147	"
5	2126.8	89.3	2196	6	AX121362	"
6	2126.8	89.3	2196	6	BD163479	Nakagawa JP doc
7	1498.4	62.9	308650	1	AP005218	
8	590.6	24.8	11785	1	AE012833	
c 9	583.6	24.5	12009	1	AE011922	
c 10	574.2	24.1	10101	1	AE012376	
11	563.8	23.7	17916	1	AE007004	
12	563.8	23.7	36030	1	MTCY50	
13	563.8	23.7	75216	6	AX704275	
14	562.2	23.6	299450	1	BX248338	
15	545	22.9	2333	1	KPNDEAD	
c 16	519.8	21.8	300029	1	AE012553	
c 17	519.6	21.8	12008	1	AE003878	
c 18	516	21.7	11002	1	AE015331	
c 19	516	21.7	292497	1	AE016989	
c 20	516	21.7	300359	1	AE016767	
c 21	514.6	21.6	14820	1	AE000397	
c 22	514.6	21.6	14820	6	AX370215	
c 23	514.6	21.6	14820	6	AX370260	
c 24	514.6	21.6	110000	1	ECOUW67_0	
c 25	513.6	21.6	110000	2	AC074221_3	Continuation (4 of
c 26	511.4	21.5	20120	1	AE008851	AE008851 Salmonell
c 27	508	21.3	10994	1	AE005544	AE005544 Escherich
c 28	508	21.3	307962	1	AP002564	AP002564 Escherich
29	500.8	21.0	2863	6	BD103627	BD103627 Method an
c 30	500.2	21.0	258050	1	AL627278	AL627278 Salmonell
c 31	500.2	21.0	301574	1	AE016844	AE016844 Salmonell
32	497.2	20.9	2982	1	EPCODEAD	M63288 E.coli deaD
c 33	468.6	19.7	11873	1	AE004710	AE004710 Pseudomon

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 17:04:44 ; Search time 633 Seconds
(without alignments)
10153.810 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
	1	2381	100.0	2381	24	AAD28043 <i>Appl. 40</i>
	2	2377.8	99.9	349980	22	AAH68527 <i>EP</i>
	3	2377.8	99.9	349980	22	AAH68528 <i>EP</i>
	4	2126.8	89.3	2196	22	AAH66243 <i>EP</i>
	5	1674	70.3	1674	25	ACA00444 DE10128510 - lots
	6	563.8	23.7	75216	24	ABX09141 <i>of seq</i>
	7	563.8	23.7	4403765	22	AAI99683
	8	563.8	23.7	4411529	22	AAI99682
	9	514.6	21.6	1941	23	AAS52577
c	10	514.6	21.6	14820	22	AAS46246
c	11	514.6	21.6	14820	22	AAS46268
	12	500.8	21.0	2863	19	AAV38314
	13	500.2	21.0	1941	23	AAS56034
	14	468.4	19.7	1704	23	AAS54151
	15	445.4	18.7	3020	23	AAS89058
c	16	442.6	18.6	1219	23	AAS81866
	17	357.6	15.0	1842	23	AAS53256
	18	357.6	15.0	1830121	17	AAT42063
c	19	295.8	12.4	640681	24	ABA92787
	20	271.4	11.4	1536	24	AAD31864
	21	269.2	11.3	1800	20	AAZ25012
	22	262	11.0	273	25	ACA00443
	23	259.4	10.9	5738	24	ABQ70978
	24	253	10.6	1163020	24	ABQ67197
	25	253	10.6	2944528	24	ABA03041
	26	253	10.6	3011208	24	ABQ69245
	27	244.8	10.3	1617	24	ABN69410
	28	242.6	10.2	2365589	24	ABA90521
	29	235.4	9.9	1575	23	AAS55756
	30	234.6	9.9	1618	18	AAT62139
	31	234.4	9.8	939	24	ABK74369
	32	233.8	9.8	1572	25	ABX07336
	33	233.8	9.8	1638	25	ABZ42472
c	34	233.8	9.8	3230	19	AAV52336
c	35	233.8	9.8	2162598	25	ABS56454
	36	233	9.8	1618	16	AAT05503
	37	233	9.8	1618	18	AAT80384
	38	233	9.8	1618	19	AAV47559
	39	233	9.8	1618	20	AAX02202
	40	233	9.8	1618	24	AAD47112
	41	233	9.8	1618	24	AAF88525
	42	233	9.8	1618	24	AAD40286
	43	233	9.8	1618	24	ABK81734
	44	233	9.8	1618	24	AAS96023
	45	223	9.4	1867	18	AAT80385

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 19:06:09 ; Search time 4971 Seconds
(without alignments)
11641.311 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaacccgcagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estmu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_htc:
9: gb_est1:
10: gb_est2:
11: gb_htc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rod:
26: em_gss_phg:
27: em_gss_vrl:

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query					Description
			Match	Length	DB	ID	%	
c	1	241	10.1	3539	28	BH770982		BH770982 LLMGtag70
	2	213.2	9.0	1101	29	BZ549647		BZ549647 pacsl-60
	3	195.4	8.2	1443	12	BM321064		BM321064 rockefell
	4	193.6	8.1	1929	11	AY104966		AY104966 Zea mays
c	5	190.6	8.0	936	29	BZ566692		BZ566692 pacss2-164
	6	190	8.0	1175	14	CD508153		CD508153 CDA89-C04
c	7	183.4	7.7	712	29	BZ549701		BZ549701 pacsl-60
	8	181.8	7.6	948	29	BZ553880		BZ553880 pacsl-60
	9	180.2	7.6	1609	11	AY109160		AY109160 Zea mays
	10	177.2	7.4	1772	11	AK077429		AK077429 Mus muscu
	11	172.8	7.3	1393	11	BC032078		BC032078 Homo sapi
	12	172.4	7.2	1793	11	BC012282		BC012282 Mus muscu
	13	172	7.2	1748	11	AK076982		AK076982 Mus muscu
	14	172	7.2	1752	11	AK010310		AK010310 Mus muscu
	15	167.4	7.0	544	28	AQ989915		AQ989915 Rfc00591
	16	167	7.0	1418	11	AK010644		AK010644 Mus muscu
	17	167	7.0	1438	11	AK075920		AK075920 Mus muscu
	18	163.6	6.9	1165	14	CD507904		CD507904 CDA87-G05
	19	163.6	6.9	1201	9	AL568646		AL568646 AL568646
	20	157	6.6	688	14	CD045220		CD045220 psHB018xI
c	21	156.8	6.6	696	28	BH143507		BH143507 TDGEA79TH
	22	155.6	6.5	786	29	BZ564147		BZ564147 pacss2-164
	23	155.6	6.5	802	13	BU476989		BU476989 603841415
	24	155.2	6.5	972	11	CNS08PRP		BX022817 Single re
	25	153	6.4	1031	11	CNS08DJ2		BX006954 Single re
	26	152.6	6.4	835	29	BZ565507		BZ565507 pacss2-164
	27	152	6.4	1012	13	BU112303		BU112303 603129440
	28	149.4	6.3	1163	14	CD497898		CD497898 CDA30-E05
	29	148.2	6.2	1201	9	AL535247		AL535247 AL535247
	30	148.2	6.2	2972	11	AK031534		AK031534 Mus muscu
	31	147.6	6.2	871	14	CD439282		CD439282 EL01N0523
	32	147	6.2	1033	11	CNS090JP		BX036785 Single re
	33	146.6	6.2	2986	11	AK028274		AK028274 Mus muscu
	34	146.6	6.2	3956	11	BC043699		BC043699 Mus muscu
	35	146.4	6.1	1629	11	AK076509		AK076509 Mus muscu
	36	145.8	6.1	704	13	BU406237		BU406237 603482292
	37	145.8	6.1	832	29	BZ718032		BZ718032 PUBNU85TD
	38	145.8	6.1	1124	13	BX384332		BX384332 BX384332
	39	145.6	6.1	980	11	CNS0941F		BX041311 Single re
c	40	145.6	6.1	1102	29	BZ559358		BZ559358 pacss2-164
	41	145	6.1	2984	11	AK031679		AK031679 Mus muscu
c	42	143.8	6.0	964	11	CNS08V7D		BX029861 Single re
	43	143.8	6.0	1018	11	CNS090FU		BX036646 Single re
	44	143.2	6.0	1151	11	AY105919		AY105919 Zea mays
c	45	142.8	6.0	924	11	CNS09HZH		BX059385 Single re

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 15:25:32 ; Search time 144 Seconds
(without alignments)
7298.147 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga.....ctctctagtcagagtgcgag 2381
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
	1	563.8	23.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	2	563.8	23.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	3	465.4	19.5	2100	4	US-09-252-991A-9660	Sequence 9660, Ap
	4	465.2	19.5	1785	4	US-09-252-991A-9701	Sequence 9701, Ap
	5	357.6	15.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
	6	357.6	15.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	7	271.4	11.4	1592	4	US-09-634-238-34	Sequence 34, Appli
	8	269.2	11.3	1800	3	US-09-039-773A-1	Sequence 1, Appli
c	9	250.6	10.5	996	4	US-09-252-991A-9594	Sequence 9594, Ap
	10	250.2	10.5	1407	4	US-09-252-991A-5967	Sequence 5967, Ap
c	11	250.2	10.5	1620	4	US-09-252-991A-5920	Sequence 5920, Ap

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 16:30:32 ; Search time 633 Seconds
(without alignments)
9760.262 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapext 1.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	2381	100.0	2381	10	US-09-963-790A-1	Appl.
2	2377.8	99.9	3309400	10	US-09-738-626-1	Nakagawa
3	2126.8	89.3	2196	10	US-09-738-626-1278	"
4	563.8	23.7	75216	15	US-10-080-170-646	
5	514.6	21.6	1941	9	US-09-815-242-6214	
6	500.2	21.0	1941	9	US-09-815-242-9671	
7	468.4	19.7	1704	9	US-09-815-242-7788	
8	357.6	15.0	1842	9	US-09-815-242-6893	
9	357.6	15.0	1830121	14	US-10-329-960-1	
c 10	295.8	12.4	640681	10	US-09-790-988-1	
11	271.4	11.4	1536	10	US-09-971-536-10	
12	247.4	10.4	2241	14	US-10-156-761-4107	
c 13	247.4	10.4	9025608	14	US-10-156-761-1	
14	235.4	9.9	1575	9	US-09-815-242-9393	
15	234.4	9.8	939	10	US-09-974-300-1660	
16	234	9.8	1506	14	US-10-156-761-4139	
17	234	9.8	9025608	14	US-10-156-761-1	
18	233	9.8	1618	9	US-09-874-923-9	
19	233	9.8	1618	10	US-09-991-496-9	
20	233	9.8	1618	12	US-10-098-732A-68	
21	230.2	9.7	1530	14	US-10-156-761-4430	
c 22	217.8	9.1	38734	11	US-09-373-658-30	
23	214.4	9.0	1449	10	US-09-974-300-6077	
24	214	9.0	1611	9	US-09-815-242-6677	
25	212.8	8.9	2293	9	US-09-842-552-85	
26	212.6	8.9	1272	10	US-09-738-626-859	
c 27	212.6	8.9	3309400	10	US-09-738-626-1	
28	202.4	8.5	2277	14	US-10-156-761-3085	
29	200	8.4	1494	14	US-10-156-761-7032	
30	187	7.9	1476	10	US-09-732-091-1	
31	187	7.9	1479	9	US-09-815-242-7211	
32	187	7.9	1512	10	US-09-732-091-41	
33	175.2	7.4	1749	10	US-09-765-231A-14	
34	174.8	7.3	1227	14	US-10-128-714-2184	
35	172.8	7.3	1383	10	US-09-864-864-294	
36	172.8	7.3	1383	12	US-10-334-038-15	
37	168.2	7.1	1266	9	US-09-815-242-7606	
38	168	7.1	1823	11	US-09-909-567B-12	
39	163.8	6.9	1245	10	US-09-938-842A-2339	
40	158.4	6.7	2437	10	US-09-833-381-1478	
41	158.4	6.7	2437	10	US-09-833-381-1479	
42	156.8	6.6	2900	14	US-10-037-270-1045	
43	153.4	6.4	1512	10	US-09-880-107-3452	
44	152.4	6.4	1682	9	US-09-755-325-7	
45	152.4	6.4	1682	12	US-10-429-997-7	

ALIGNMENTS

RESULT 1
US-09-963-790A-1

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 23:28:21 ; Search time 8732 Seconds
(without alignments)
11155.041 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:

```

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	2381	100.0	2381	6	AX404864	AX404864 Sequence
2	2279	95.7	333150	1	AP005277	AP005277 Corynebac
3	2279	95.7	349980	6	AX127146	AX127146 Sequence
4	2279	95.7	349980	6	AX127147	AX127147 Sequence
5	2028	85.2	2196	6	AX121362	AX121362 Sequence
6	2028	85.2	2196	6	BD163479	BD163479 Novel pol
7	44	1.8	308650	1	AP005218	AP005218 Corynebac
c 8	26	1.1	10101	1	AE012376	AE012376 Xanthomon
c 9	24	1.0	12514	1	AE012011	AE012011 Xanthomon
c 10	24	1.0	320150	1	AP005033	AP005033 Streptomy
c 11	23	1.0	10491	1	AE005859	AE005859 Caulobact
c 12	23	1.0	12039	1	AE009534	AE009534 Brucella
c 13	23	1.0	12080	1	AE014406	AE014406 Brucella
c 14	23	1.0	109911	2	AC118330_4	Continuation (5 of
c 15	23	1.0	190050	1	AL646059	AL646059 Ralstonia
c 16	23	1.0	198050	1	AL646061	AL646061 Ralstonia
c 17	23	1.0	217794	2	AC111124	AC111124 Mus muscu
c 18	23	1.0	237801	2	AC137306	AC137306 Rattus no
c 19	23	1.0	238039	2	AC137290	AC137290 Rattus no
c 20	23	1.0	311000	1	SCO939122	AL939122 Streptomy
c 21	23	1.0	311583	2	AC105794	AC105794 Rattus no
c 22	23	1.0	347660	1	AP002994	AP002994 Mesorhizo
c 23	23	1.0	347660	1	AP002994	AP002994 Mesorhizo
c 24	22	0.9	198	6	AX313944	AX313944 Sequence
c 25	22	0.9	301675	1	AP005027	AP005027 Streptomy
c 26	21	0.9	28	6	AX404866	AX404866 Sequence
c 27	21	0.9	28	6	AX404867	AX404867 Sequence
c 28	21	0.9	10652	6	AX344648	AX344648 Sequence
c 29	21	0.9	12312	1	AE012307	AE012307 Xanthomon
c 30	21	0.9	158944	9	AC096746	AC096746 Homo sapi
c 31	21	0.9	159878	2	AC124143	AC124143 Oryza sat
c 32	21	0.9	187002	2	AC134483	AC134483 Rattus no
c 33	21	0.9	192234	2	AC132132	AC132132 Mus muscu

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 22:02:48 ; Search time 634 Seconds
(without alignments)
10137.795 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgcagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	
	1	2381	100.0	2381	24	AAD28043	Corynebacterium gl
	2	2279	95.7	349980	22	AAH68527	C glutamicum codin
	3	2279	95.7	349980	22	AAH68528	C glutamicum codin
	4	2028	85.2	2196	22	AAH66243	C glutamicum codin
	5	1674	70.3	1674	25	ACA00444	C. glutamicum codin
	6	184	7.7	273	25	ACA00443	C. glutamicum deri
	7	22	0.9	198	24	ABN78518	C. glutamicum deri
c	8	21	0.9	28	24	AAD28045	Human helicase-lik
c	9	21	0.9	10652	24	ABN80056	Corynebacterium gl
c	10	20	0.8	1219	23	AAS81866	Human chemically m
	11	20	0.8	1266	23	AAS53969	DNA encoding novel
c	12	20	0.8	1584	22	AAS57165	Klebsiella pneumon
c	13	20	0.8	1584	23	ABL19907	cDNA encoding Dros
	14	20	0.8	1584	24	ABN69409	Drosophila melanog
	15	20	0.8	1584	24	ABN70539	Streptococcus poly
	16	20	0.8	1941	23	AAS52577	Streptococcus poly
	17	20	0.8	2863	19	AAV38314	E. coli DNA for ce
	18	20	0.8	3020	23	AAS89058	Nucleotide sequenc
	19	20	0.8	3117	23	AAS73364	DNA encoding novel
	20	20	0.8	3117	23	AAS89055	DNA encoding novel
	21	20	0.8	3117	23	AAS92864	DNA encoding novel
	22	20	0.8	4185	22	AAS57164	DNA encoding Dros
	23	20	0.8	4185	23	ABL19906	Drosophila melanog
c	24	20	0.8	14820	22	AAS46246	DNA encoding novel
c	25	20	0.8	14820	22	AAS46268	DNA encoding novel
	26	20	0.8	68750	21	AAZ55887	Sorangium cellulos
	27	20	0.8	71989	21	AAA29349	Sorangium cellulos
	28	20	0.8	2155561	24	ABN71527	Streptococcus poly
	29	19	0.8	28	24	AAD28044	Corynebacterium gl
c	30	19	0.8	346	21	AAC74485	Human ORFX ORF40 p
c	31	19	0.8	346	24	ABN16048	Human ORFX polynuc
	32	19	0.8	515	24	ABK62676	Rat sequence diffe
c	33	19	0.8	520	19	AAV47569	Leishmania antigen
c	34	19	0.8	520	24	AAF88535	L. major LmgSP1 an
c	35	19	0.8	520	24	AAD40296	Leishmania major L
c	36	19	0.8	520	24	ABK81742	Leishmania antigen
c	37	19	0.8	520	24	AAS96033	Leishmania antigen
	38	19	0.8	557	24	ABK62433	Rat sequence diffe
	39	19	0.8	1371	23	ABL24281	Drosophila melanog
	40	19	0.8	1941	23	AAS56034	Salmonella typhi D
	41	19	0.8	4079	25	ACA56639	Human signalling p
	42	19	0.8	4839	25	ABZ42531	Human neuromedin K
	43	19	0.8	5137	23	ABL24280	Drosophila melanog
c	44	19	0.8	5760	24	ABS78661	M. echinospora DNA
	45	19	0.8	5871	24	ABS78666	S. ghanaensis DNA

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:07:32 ; Search time 4971 Seconds
(without alignments)
11641.311 Million cell updates/sec

Title: US-09-963-790A-1

Perfect score: 2381

Sequence: 1 caggaaaccccgagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:
 29: gb_gss2:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	%	Description
							Query	
	1	22	0.9	471	9	AU284741		AU284741 AU284741
	2	22	0.9	562	12	BJ411196		BJ411196 BJ411196
	3	22	0.9	631	9	AU268561		AU268561 AU268561
c	4	22	0.9	660	12	BM634053		BM634053 170006688
c	5	22	0.9	714	12	BM656204		BM656204 170006873
c	6	21	0.9	573	13	BU543982		BU543982 GM880001A
	7	21	0.9	575	29	BZ345001		BZ345001 hr43d08.b
	8	21	0.9	606	12	BM603218		BM603218 170006870
	9	21	0.9	612	28	AZ418854		AZ418854 1M0195C09
	10	21	0.9	715	13	BU634805		BU634805 018D02 In
	11	21	0.9	848	10	BF260369		BF260369 HVSMEf002
c	12	20	0.8	160	28	AZ921472		AZ921472 1006030B0
c	13	20	0.8	275	12	BI674592		BI674592 949022D11
	14	20	0.8	305	9	AA571940		AA571940 vg12d02.r
c	15	20	0.8	327	28	BH228484		BH228484 1006147C0
c	16	20	0.8	330	28	BH228575		BH228575 1006147F0
c	17	20	0.8	340	28	BH217878		BH217878 1006060G0
	18	20	0.8	344	13	BQ760997		BQ760997 EBro04 SQ
c	19	20	0.8	344	28	BH216414		BH216414 1006042E0
c	20	20	0.8	351	28	BH217881		BH217881 1006060G0
c	21	20	0.8	352	28	AZ921694		AZ921694 1006031E0
c	22	20	0.8	352	28	BH216419		BH216419 1006042E0
c	23	20	0.8	352	28	BH228573		BH228573 1006147F0
c	24	20	0.8	353	28	BH228482		BH228482 1006147C0
c	25	20	0.8	355	28	BH228632		BH228632 1006147H0
	26	20	0.8	363	13	BQ993892		BQ993892 QGF5M01.y
	27	20	0.8	383	9	AW417369		AW417369 53455 MAR
	28	20	0.8	385	9	AW115311		AW115311 rs65e07.y
	29	20	0.8	393	9	AW307746		AW307746 1617 MARC
	30	20	0.8	410	12	BI336407		BI336407 AR095H07S
	31	20	0.8	482	10	BE481452		BE481452 166898 BA
	32	20	0.8	484	12	BM106031		BM106031 509650 MA
c	33	20	0.8	494	28	BH216148		BH216148 1006040F0
	34	20	0.8	497	14	CB287818		CB287818 CMD67_F04
	35	20	0.8	528	10	BE233269		BE233269 139379 MA
	36	20	0.8	532	10	BE234987		BE234987 142387 MA
	37	20	0.8	532	12	BG841542		BG841542 MEST22-H0
	38	20	0.8	554	12	BM132263		BM132263 TgESTzyb0
	39	20	0.8	558	9	AV601072		AV601072 AV601072
	40	20	0.8	562	12	BG834242		BG834242 352389 MA
	41	20	0.8	580	9	AW097037		AW097037 rs31h08.y
c	42	20	0.8	584	14	CD484986		CD484986 3529_1_11
	43	20	0.8	600	14	CB455480		CB455480 712623 MA
	44	20	0.8	608	12	BM078668		BM078668 MEST122-G
	45	20	0.8	614	10	BE205350		BE205350 EST398026

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 19:17:14 ; Search time 144 Seconds
(without alignments)
7298.147 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaacccgcagggtga.....ctctctagtcagagtgcgag 2381
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
<hr/>						
c 1	20	0.8	483	4	US-09-252-991A-5687	Sequence 5687, Ap
c 2	20	0.8	2328	4	US-09-252-991A-5729	Sequence 5729, Ap
c 3	20	0.8	4230	4	US-09-252-991A-5711	Sequence 5711, Ap
c 4	20	0.8	4941	4	US-09-252-991A-5741	Sequence 5741, Ap
c 5	20	0.8	68750	3	US-09-335-409-1	Sequence 1, Appli
c 6	20	0.8	68750	4	US-09-568-102-1	Sequence 1, Appli
c 7	20	0.8	68750	4	US-09-567-969-1	Sequence 1, Appli
c 8	20	0.8	68750	4	US-09-568-480-1	Sequence 1, Appli
c 9	20	0.8	68750	4	US-09-568-486-1	Sequence 1, Appli
c 10	20	0.8	68750	4	US-09-568-472-1	Sequence 1, Appli
c 11	20	0.8	68750	4	US-09-567-899-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 23:25:50 ; Search time 632 Seconds
(without alignments)
9775.705 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 cagggaaaccccgcagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1731049 seqs, 1297405648 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
	1	2381	100.0	2381	10	US-09-963-790A-1	Sequence 1, Appli
	2	2279	95.7	3309400	10	US-09-738-626-1	Sequence 1, Appli
	3	2028	85.2	2196	10	US-09-738-626-1278	Sequence 1278, Ap
	4	24	1.0	2064	14	US-10-156-761-2902	Sequence 2902, Ap
	5	24	1.0	125746	14	US-10-156-761-15102	Sequence 15102, A
c	6	24	1.0	9025608	14	US-10-156-761-1	Sequence 1, Appli
	7	22	0.9	603	14	US-10-156-761-1568	Sequence 1568, Ap
	8	21	0.9	28	10	US-09-963-790A-3	Sequence 3, Appli
c	9	21	0.9	28	10	US-09-963-790A-4	Sequence 4, Appli
c	10	20	0.8	503	11	US-09-918-995-34274	Sequence 34274, A
	11	20	0.8	1266	9	US-09-815-242-7606	Sequence 7606, Ap
c	12	20	0.8	1584	14	US-10-270-333-140	Sequence 140, App
	13	20	0.8	1941	9	US-09-815-242-6214	Sequence 6214, Ap
	14	20	0.8	4185	14	US-10-270-333-139	Sequence 139, App
	15	20	0.8	68750	13	US-10-014-717-1	Sequence 1, Appli
	16	19	0.8	480	10	US-09-991-496-132	Sequence 132, App
	17	19	0.8	515	10	US-09-917-800A-583	Sequence 583, App
c	18	19	0.8	520	9	US-09-874-923-29	Sequence 29, Appli
c	19	19	0.8	520	10	US-09-991-496-29	Sequence 29, Appli
	20	19	0.8	522	14	US-10-156-761-2688	Sequence 2688, Ap
	21	19	0.8	546	14	US-10-156-761-1619	Sequence 1619, Ap
	22	19	0.8	557	10	US-09-917-800A-340	Sequence 340, App
	23	19	0.8	561	14	US-10-156-761-3799	Sequence 3799, Ap
c	24	19	0.8	1137	14	US-10-156-761-6123	Sequence 6123, Ap
c	25	19	0.8	1495	10	US-09-991-496-133	Sequence 133, App
	26	19	0.8	1941	9	US-09-815-242-9671	Sequence 9671, Ap
c	27	19	0.8	2613	14	US-10-156-761-6694	Sequence 6694, Ap
	28	19	0.8	4839	14	US-10-225-567A-544	Sequence 544, App
	29	19	0.8	75216	15	US-10-080-170-646	Sequence 646, App
	30	19	0.8	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	31	18	0.8	273	9	US-09-294-093B-2452	Sequence 2452, Ap
	32	18	0.8	287	9	US-09-294-093B-2110	Sequence 2110, Ap
	33	18	0.8	453	13	US-10-027-632-45454	Sequence 45454, A
c	34	18	0.8	511	10	US-09-783-590-5786	Sequence 5786, Ap
	35	18	0.8	576	14	US-10-156-761-2684	Sequence 2684, Ap
	36	18	0.8	577	13	US-10-027-632-60237	Sequence 60237, A
	37	18	0.8	577	13	US-10-027-632-298225	Sequence 298225,
	38	18	0.8	603	14	US-10-156-761-6940	Sequence 6940, Ap
	39	18	0.8	624	14	US-10-156-761-2946	Sequence 2946, Ap
	40	18	0.8	630	13	US-10-027-632-85667	Sequence 85667, A
	41	18	0.8	630	13	US-10-027-632-109733	Sequence 109733,
	42	18	0.8	630	13	US-10-027-632-315189	Sequence 315189,
	43	18	0.8	630	13	US-10-027-632-315190	Sequence 315190,
c	44	18	0.8	877	13	US-10-027-632-10098	Sequence 10098, A
	45	18	0.8	966	14	US-10-156-761-3002	Sequence 3002, Ap

ALIGNMENTS

RESULT 1
US-09-963-790A-1

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 09:38:47 ; Search time 6356 Seconds
(without alignments)
4016.301 Million cell updates/sec

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVGYETPSPI.....RGRDDRGDRGGRGGYRGGRD 624

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152711_1464/app_query.fasta_1.77
5
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09963790_@CGN_1_1_3963_@runat_14102003_152711_1464 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:

```

11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*
15:  em_ba:*
16:  em_fun:*
17:  em_hum:*
18:  em_in:*
19:  em_mu:*
20:  em_om:*
21:  em_or:*
22:  em_ov:*
23:  em_pat:*
24:  em_ph:*
25:  em_pl:*
26:  em_ro:*
27:  em_sts:*
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
%						
1	3187	99.9	2381	6	AX404864	AX404864 Sequence
2	3180	99.7	2196	6	AX121362	AX121362 Sequence
3	3180	99.7	2196	6	BD163479	BD163479 Novel pol
4	3180	99.7	333150	1	AP005277	AP005277 Corynebac
5	3180	99.7	349980	6	AX127146	AX127146 Sequence
6	3180	99.7	349980	6	AX127147	AX127147 Sequence
7	2825	88.6	308650	1	AP005218	AP005218 Corynebac
8	1669.5	52.3	299450	1	BX248338	BX248338 Mycobacte
9	1667.5	52.3	17916	1	AE007004	AE007004 Mycobacte
10	1667.5	52.3	36030	1	MTCY50	Z77137 Mycobacteri
11	1667.5	52.3	75216	6	AX704275	AX704275 Sequence
c 12	1587	49.7	12009	1	AE011922	AE011922 Xanthomon
c 13	1584.5	49.7	10101	1	AE012376	AE012376 Xanthomon
14	1527	47.9	11785	1	AE012833	AE012833 Chlorobi
c 15	1520	47.6	300029	1	AE012553	AE012553 Xylella f
c 16	1511.5	47.4	12008	1	AE003878	AE003878 Xylella f

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 09:38:57 ; Search time 447 Seconds
(without alignments)
3768.343 Million cell updates/sec

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVGYETPSPI.....RGRDDRGDRGGRRGGYRGGRD 624

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152711_1428/app_query.fasta_1.77
5
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09963790_@CGN_1_1_0_@runat_14102003_152711_1428 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : N_Geneseq_19Jun03:*

```
1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
```

```

11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
%						
	1	3187	99.9	2381	24	AAD28043 Corynebacterium gl
	2	3180	99.7	2196	22	CAAH66243 C glutamicum codin
	3	3180	99.7	349980	22	AAH68527 C glutamicum codin
	4	3180	99.7	349980	22	AAH68528 C glutamicum codin
	5	2865	89.8	1674	25	ACA00444 C. glutamicum deri
	6	1667.5	52.3	75216	24	ABX09141 Mycobacterium tube
	7	1667.5	52.3	4403765	22	AAI999683 Mycobacterium tube
	8	1667.5	52.3	4411529	22	AAI999682 Mycobacterium tube
	9	1423.5	44.6	1941	23	AAS52577 E. coli DNA for ce
c	10	1423.5	44.6	14820	22	AAS46246 DNA encoding novel
c	11	1423.5	44.6	14820	22	AAS46268 DNA encoding novel
	12	1422.5	44.6	1941	23	AAS56034 Salmonella typhi D
	13	1391.5	43.6	2863	19	AAV38314 Nucleotide sequenc
	14	1333.5	41.8	1842	23	AAS53256 Haemophilus influe
	15	1333.5	41.8	1830121	17	AAT42063 Haemophilus influe
c	16	1300	40.8	640681	24	ABA92787 Buchnera sp. genom
	17	1200.5	37.6	1704	23	AAS54151 Pseudomonas aerugi
	18	1118	35.0	3020	23	AAS89058 DNA encoding novel
c	19	1113	34.9	1219	23	AAS81866 DNA encoding novel
	20	980	30.7	1449	24	ABK78786 Bacillus clausii g
	21	974	30.5	1584	24	ABN69409 Streptococcus poly
	22	974	30.5	1584	24	ABN70539 Streptococcus poly
	23	974	30.5	2155561	24	ABN71527 Streptococcus poly
	24	962.5	30.2	2365589	24	ABA90521 Genomic sequence o
	25	958.5	30.0	2944528	24	ABA03041 Listeria monocytog
	26	956.5	30.0	1617	24	ABN69410 Streptococcus poly
	27	952.5	29.9	5738	24	ABQ70978 Listeria monocytog
	28	950	29.8	1163020	24	ABQ67197 Listeria innocua c
	29	950	29.8	3011208	24	ABQ69245 Listeria innocua D
	30	912.5	28.6	1611	23	AAS53040 Enterococcus faeca
	31	906	28.4	1572	25	ABX07336 S. pneumoniae type
	32	906	28.4	1575	23	AAS55756 Streptococcus pneu

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 09:38:44 ; Search time 3488 Seconds
(without alignments)
4348.048 Million cell updates/sec

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVGYETPSPI.....RGRDDRGDRGGRGGYRGGRD 624

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152712_1487/app_query.fasta_1.77
5
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09963790@CGN_1_1_2810@runat_14102003_152712_1487 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estmu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_htc:
9: gb_est1:
10: gb_est2:

```

11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
c 1	922.5	28.9	3539	28	BH770982	BH770982 LLMGtag ⁷⁰
2	703.5	22.1	2376	11	AK030239	AK030239 Mus muscu
3	703.5	22.1	2517	11	BC049906	BC049906 Mus muscu
4	703.5	22.1	2638	11	AK041281	AK041281 Mus muscu
5	680	21.3	2756	11	AK010281	AK010281 Mus muscu
6	680	21.3	4723	11	BC043655	BC043655 Mus muscu
7	674.5	21.1	1393	11	BC032078	BC032078 Homo sapi
8	674.5	21.1	1772	11	AK077429	AK077429 Mus muscu
9	674.5	21.1	1793	11	BC012282	BC012282 Mus muscu
10	671.5	21.1	3212	11	AK029542	AK029542 Mus muscu
11	669.5	21.0	1629	11	AK076509	AK076509 Mus muscu
12	669	21.0	1438	11	AK075920	AK075920 Mus muscu
13	668	20.9	2321	11	BC046554	BC046554 Mus muscu
14	668	20.9	2329	11	AK088887	AK088887 Mus muscu
15	664.5	20.8	4014	11	AK049311	AK049311 Mus muscu
16	664	20.8	3313	11	BC009432	BC009432 Homo sapi
17	663.5	20.8	1748	11	AK076982	AK076982 Mus muscu
18	663.5	20.8	1752	11	AK010310	AK010310 Mus muscu
19	660	20.7	2329	11	AK044792	AK044792 Mus muscu
20	658	20.6	4626	11	BC007668	BC007668 Homo sapi
21	651	20.4	1609	11	AY109160	AY109160 Zea mays
22	649.5	20.4	1929	11	AY104966	AY104966 Zea mays
23	641.5	20.1	1418	11	AK010644	AK010644 Mus muscu
24	641	20.1	1902	11	BC006469	BC006469 Homo sapi
25	638	20.0	3031	11	BC051046	BC051046 Mus muscu
26	625	19.6	2338	11	AK076018	AK076018 Mus muscu
27	619.5	19.4	1443	12	BM321064	BM321064 rockefell
28	619	19.4	1201	9	AL568646	AL568646 AL568646

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 12:06:29 ; Search time 100 Seconds
(without alignments)
2754.231 Million cell updates/sec

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVGYETPSPI.....RGRDDRGDRGGRRGGYRGGRD 624

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152709_1336/app_query.fasta_1.77
5
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09963790_@CGN_1_1_56_@runat_14102003_152709_1336 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Issued_Patents_NA:*

```
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
	1	1667.5	52.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	2	1667.5	52.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	3	1333.5	41.8	1830121	4	US-09-557-884-1	Sequence 1, Appli
	4	1333.5	41.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	5	1201	37.6	2100	4	US-09-252-991A-9660	Sequence 9660, Ap
	6	1200.5	37.6	1785	4	US-09-252-991A-9701	Sequence 9701, Ap
c	7	906	28.4	3230	4	US-08-961-527-203	Sequence 203, App
	8	904	28.3	1533	4	US-09-107-532A-2328	Sequence 2328, Ap
	9	897.5	28.1	1800	3	US-09-039-773A-1	Sequence 1, Appli
	10	895	28.1	1592	4	US-09-634-238-34	Sequence 34, Appli
	11	848	26.6	1587	4	US-09-134-001C-1425	Sequence 1425, Ap
	12	790.5	24.8	1941	4	US-09-328-352-1891	Sequence 1891, Ap
	13	786	24.6	1407	4	US-09-252-991A-5967	Sequence 5967, Ap
c	14	786	24.6	1620	4	US-09-252-991A-5920	Sequence 5920, Ap
c	15	783	24.5	4774	4	US-09-221-017B-1	Sequence 1, Appli
	16	769.5	24.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	17	723.5	22.7	1488	4	US-09-252-991A-421	Sequence 421, App
	18	716.5	22.5	1374	3	US-08-929-738-1	Sequence 1, Appli
	19	716.5	22.5	1614	3	US-08-929-738-2	Sequence 2, Appli
	20	687	21.5	3288	4	US-09-844-521-3	Sequence 3, Appli
	21	687	21.5	3304	4	US-09-620-312D-105	Sequence 105, App
	22	685	21.5	1383	4	US-09-252-991A-5684	Sequence 5684, Ap
c	23	685	21.5	1557	4	US-09-252-991A-5539	Sequence 5539, Ap
c	24	683	21.4	1830121	4	US-09-557-884-1	Sequence 1, Appli
c	25	683	21.4	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	26	676	21.2	1682	3	US-09-318-443-7	Sequence 7, Appli
	27	673	21.1	1536	3	US-09-318-443-5	Sequence 5, Appli
	28	663.5	20.8	1254	5	PCT-US96-05320A-894	Sequence 894, App
	29	662	20.8	1245	3	US-09-318-443-1	Sequence 1, Appli
	30	661	20.7	2319	3	US-09-058-489-90	Sequence 90, Appli
	31	661	20.7	4416	3	US-09-058-489-17	Sequence 17, Appli
	32	658.5	20.6	3408	3	US-09-058-489-14	Sequence 14, Appli
	33	658.5	20.6	5322	3	US-09-058-489-13	Sequence 13, Appli
	34	653	20.5	3825	3	US-09-208-742-3	Sequence 3, Appli
c	35	652	20.4	1602	4	US-09-252-991A-3776	Sequence 3776, Ap
	36	652	20.4	1755	4	US-09-252-991A-3588	Sequence 3588, Ap
	37	652	20.4	1867	2	US-08-607-509-3	Sequence 3, Appli
	38	652	20.4	1867	2	US-08-634-642-3	Sequence 3, Appli
	39	652	20.4	1867	3	US-08-989-370-3	Sequence 3, Appli
	40	649	20.3	3347	4	US-09-702-705-318	Sequence 318, App
	41	649	20.3	3347	4	US-09-736-457-318	Sequence 318, App
	42	645.5	20.2	1116	4	US-09-252-991A-5946	Sequence 5946, Ap
	43	644	20.2	1281	4	US-09-252-991A-3691	Sequence 3691, Ap
	44	640	20.1	1618	2	US-08-533-669A-9	Sequence 9, Appli
	45	640	20.1	1618	2	US-08-607-509-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-103-840A-2

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 11:02:43 ; Search time 1123 Seconds
(without alignments)
1441.819 Million cell updates/sec

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVGYETPSPI.....RGRDDRGDRGGRGGYRGGRD 624

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152710_1373/app_query.fasta_1.77
5
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09963790@CGN_1_1_271@runat_14102003_152710_1373
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	ID
	1	3187	99.9	2381	10	US-09-963-790A-1
	2	3180	99.7	2196	10	US-09-738-626-1278
	3	3180	99.7	3309400	10	US-09-738-626-1
	4	1667.5	52.3	75216	15	US-10-080-170-646
	5	1423.5	44.6	1941	9	US-09-815-242-6214
	6	1422.5	44.6	1941	9	US-09-815-242-9671
	7	1333.5	41.8	1842	9	US-09-815-242-6893
	8	1333.5	41.8	1830121	14	US-10-329-960-1
c	9	1300	40.8	640681	10	US-09-790-988-1
	10	1200.5	37.6	1704	9	US-09-815-242-7788
	11	980	30.7	1449	10	US-09-974-300-6077
	12	912.5	28.6	1611	9	US-09-815-242-6677
	13	906	28.4	1575	9	US-09-815-242-9393
	14	898	28.2	1536	10	US-09-971-536-10
	15	866.5	27.2	2241	14	US-10-156-761-4107
c	16	866.5	27.2	9025608	14	US-10-156-761-1
	17	841	26.4	2293	9	US-09-842-552-85
	18	840	26.3	1677	10	US-09-925-637-73
	19	840	26.3	1677	14	US-10-084-205-73
	20	839	26.3	1530	9	US-09-815-242-4201
	21	836	26.2	9025608	14	US-10-156-761-1
	22	835	26.2	1464	9	US-09-815-242-8299
	23	835	26.2	1464	9	US-09-815-242-8893
	24	823	25.8	2799	9	US-09-902-627-2
	25	822	25.8	7363	8	US-08-781-986A-19
	26	812.5	25.5	1476	10	US-09-732-091-1
	27	812.5	25.5	1479	9	US-09-815-242-7211
	28	812.5	25.5	1512	10	US-09-732-091-41
	29	804	25.2	2277	14	US-10-156-761-3085
	30	714	22.4	1833	10	US-09-938-842A-1839
	31	710.5	22.3	1272	10	US-09-738-626-859
c	32	710.5	22.3	3309400	10	US-09-738-626-1
	33	704	22.1	1860	10	US-09-938-842A-699
	34	691.5	21.7	1227	14	US-10-128-714-2184
	35	690	21.6	3501	10	US-09-938-842A-13
	36	689.5	21.6	3352	14	US-10-128-714-184
	37	687	21.5	3304	14	US-10-037-270-105
	38	687	21.5	4689	9	US-09-895-652-10
	39	684.5	21.5	4105	14	US-10-128-714-551
	40	684.5	21.5	4105	14	US-10-128-714-5551